==========

Sequence Listing could not be accepted.
If you need help call the Patent Electronic Business Center at (866) 217-9197 (toll free).
Reviewer: Anne Corrigan
Timestamp: [year=2009; month=10; day=27; hr=8; min=42; sec=23; ms=108;]

==========

****

Reviewer Comments:
<210> 137
<211> 556
<212> PRT
<213> Artificial Sequence

<220>
<223> PDK1 - lys76 to ala

<400> 137

As an explanation of "Artificial Sequence", the above <223> response should only show "PDK1" (and, if possible, more information regarding the source of the genetic material). The "lys76 to ala" portion should go in its own <220>-<223> section.

<210> 138
<211> 556
<212> PRT
<213> Artificial Sequence

<220>
<223> Arg131 changed to alanine

The above <223> response is not a valid explanation of "Artificial Sequence"; please furnish a separate <220>-<223> section explaining "Artificial Sequence": please clearly indicate the source of the genetic material. Same type of error in Sequences 139-143.

****

Validated By CRFValidator v 1.0.3

Application No: 10517225 Version No: 1.0

Input Set:

Output Set:

Started: 2009-10-09 19:08:43.555
Finished: 2009-10-09 19:08:49.734
Elapsed: 0 hr(s) 0 min(s) 6 sec(s) 179 ms
Total Warnings: 32
Total Errors: 0
No. of SeqIDs Defined: 143
Actual SeqID Count: 143

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W	213	Artificial or Unknown found in <213> in SEQ ID (11)
W	213	Artificial or Unknown found in <213> in SEQ ID (41)
W	213	Artificial or Unknown found in <213> in SEQ ID (42)
W	213	Artificial or Unknown found in <213> in SEQ ID (43)
W	213	Artificial or Unknown found in <213> in SEQ ID (44)
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Input Set:

Output Set:

Started: 2009-10-09 19:08:43.555
Finished: 2009-10-09 19:08:49.734
Elapsed: 0 hr(s) 0 min(s) 6 sec(s) 179 ms
Total Warnings: 32
Total Errors: 0
No. of SeqIDs Defined: 143
Actual SeqID Count: 143

Error code	Error Description
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SEQUENCE LISTING

<110> ALESSI, Dario
BIONDI, Ricardo
KOMANDER, David
VAN, Aalten, Daan

<120> Methods

<130> ERP01.005APC

<140> 10517225
<141> 2009-10-09

<150> PCT/GB2003/002509
<151> 2003-06-09

<150> GB0213186.0
<151> 2002-06-08

<160> 143

<170> PatentIn version 3.1

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<213> Homo sapiens

<220>
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<222> (2)..(3)
<223> Any amino acid

<400> 1

Phe Xaa Xaa Phe
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<210> 2
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<212> PRT
<213> Homo sapiens

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<222> (2)..(3)
<223> Any residue

<220>
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<222> (5)..(5)

<223> S or T

<400> 2

Phe Xaa Xaa Phe Xaa Tyr
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<210> 3
<211> 556
<212> PRT
<213> Homo sapiens

<400> 3

Met Ala Arg Thr Thr Ser Gln Leu Tyr Asp Ala Val Pro Ile Gln Ser
1 5 10 15

Ser Val Val Leu Cys Ser Cys Pro Ser Pro Ser Met Val Arg Thr Gln
20 25 30

Thr Glu Ser Ser Thr Pro Pro Gly Ile Pro Gly Gly Ser Arg Gln Gly
35 40 45

Pro Ala Met Asp Gly Thr Ala Ala Glu Pro Arg Pro Gly Ala Gly Ser
50 55 60

Leu Gln His Ala Gln Pro Pro Pro Gln Pro Arg Lys Lys Arg Pro Glu
65 70 75 80

Asp Phe Lys Phe Gly Lys Ile Leu Gly Glu Gly Ser Phe Ser Thr Val
85 90 95

Val Leu Ala Arg Glu Leu Ala Thr Ser Arg Glu Tyr Ala Ile Lys Ile
100 105 110

Leu Glu Lys Arg His Ile Ile Lys Glu Asn Lys Val Pro Tyr Val Thr
115 120 125

Arg Glu Arg Asp Val Met Ser Arg Leu Asp His Pro Phe Phe Val Lys
130 135 140

Leu Tyr Phe Thr Phe Gln Asp Asp Glu Lys Leu Tyr Phe Gly Leu Ser
145 150 155 160

Tyr Ala Lys Asn Gly Glu Leu Leu Lys Tyr Ile Arg Lys Ile Gly Ser

```
                165                 170                 175

Phe Asp Glu Thr Cys Thr Arg Phe Tyr Thr Ala Glu Ile Val Ser Ala
            180                 185                 190

Leu Glu Tyr Leu His Gly Lys Gly Ile Ile His Arg Asp Leu Lys Pro
        195                 200                 205

Glu Asn Ile Leu Leu Asn Glu Asp Met His Ile Gln Ile Thr Asp Phe
    210                 215                 220

Gly Thr Ala Lys Val Leu Ser Pro Glu Ser Lys Gln Ala Arg Ala Asn
225                 230                 235                 240

Ser Phe Val Gly Thr Ala Gln Tyr Val Ser Pro Glu Leu Leu Thr Glu
                245                 250                 255

Lys Ser Ala Cys Lys Ser Ser Asp Leu Trp Ala Leu Gly Cys Ile Ile
            260                 265                 270

Tyr Gln Leu Val Ala Gly Leu Pro Pro Phe Arg Ala Gly Asn Glu Tyr
        275                 280                 285

Leu Ile Phe Gln Lys Ile Ile Lys Leu Glu Tyr Asp Phe Pro Glu Lys
    290                 295                 300

Phe Phe Pro Lys Ala Arg Asp Leu Val Glu Lys Leu Leu Val Leu Asp
305                 310                 315                 320

Ala Thr Lys Arg Leu Gly Cys Glu Glu Met Glu Gly Tyr Gly Pro Leu
                325                 330                 335

Lys Ala His Pro Phe Phe Glu Ser Val Thr Trp Glu Asn Leu His Gln
            340                 345                 350

Gln Thr Pro Pro Lys Leu Thr Ala Tyr Leu Pro Ala Met Ser Glu Asp
        355                 360                 365

Asp Glu Asp Cys Tyr Gly Asn Tyr Asp Asn Leu Leu Ser Gln Phe Gly
    370                 375                 380

Cys Met Gln Val Ser Ser Ser Ser Ser Ser His Ser Leu Ser Ala Ser
385                 390                 395                 400
```

```
Asp Thr Gly Leu Pro Gln Arg Ser Gly Ser Asn Ile Glu Gln Tyr Ile
                405                 410                 415

His Asp Leu Asp Ser Asn Ser Phe Glu Leu Asp Leu Gln Phe Ser Glu
            420                 425                 430

Asp Glu Lys Arg Leu Leu Leu Glu Lys Gln Ala Gly Gly Asn Pro Trp
        435                 440                 445

His Gln Phe Val Glu Asn Asn Leu Ile Leu Lys Met Gly Pro Val Asp
    450                 455                 460

Lys Arg Lys Gly Leu Phe Ala Arg Arg Arg Gln Leu Leu Leu Thr Glu
465                 470                 475                 480

Gly Pro His Leu Tyr Tyr Val Asp Pro Val Asn Lys Val Leu Lys Gly
                485                 490                 495

Glu Ile Pro Trp Ser Gln Glu Leu Arg Pro Glu Ala Lys Asn Phe Lys
            500                 505                 510

Thr Phe Phe Val His Thr Pro Asn Arg Thr Tyr Tyr Leu Met Asp Pro
        515                 520                 525

Ser Gly Asn Ala His Lys Trp Cys Arg Lys Ile Gln Glu Val Trp Arg
    530                 535                 540

Gln Arg Tyr Gln Ser His Pro Asp Ala Ala Val Gln
545                 550                 555
```

<210> 4
<211> 249
<212> PRT
<213> Homo sapiens

<400> 4

```
Met Asp Gly Thr Ala Ala Glu Pro Arg Pro Gly Ala Gly Ser Leu Gln
1               5                   10                  15

His Ala Gln Pro Pro Pro Gln Pro Arg Lys Lys Arg Pro Glu Asp Phe
            20                  25                  30
```

```
Lys Phe Gly Lys Ile Leu Gly Glu Gly Ser Phe Ser Thr Val Val Leu
        35                  40                  45

Ala Arg Glu Leu Ala Thr Ser Arg Glu Tyr Ala Ile Lys Ile Leu Glu
    50                  55                  60

Lys Arg His Ile Ile Lys Glu Asn Lys Val Pro Tyr Val Thr Arg Glu
65                  70                  75                  80

Arg Asp Val Met Ser Arg Leu Asp His Pro Phe Phe Val Lys Leu Tyr
                85                  90                  95

Phe Thr Phe Gln Asp Asp Glu Lys Leu Tyr Phe Gly Leu Ser Tyr Ala
            100                 105                 110

Lys Asn Gly Glu Leu Leu Lys Tyr Ile Arg Lys Ile Gly Ser Phe Asp
        115                 120                 125

Glu Thr Cys Thr Arg Phe Tyr Thr Ala Glu Ile Val Ser Ala Leu Glu
    130                 135                 140

Tyr Leu His Gly Lys Gly Ile Ile His Arg Asp Leu Lys Pro Glu Asn
145                 150                 155                 160

Ile Leu Leu Asn Glu Asp Met His Ile Gln Ile Thr Asp Phe Gly Thr
                165                 170                 175

Ala Lys Val Leu Ser Pro Glu Ser Lys Gln Ala Arg Ala Asn Ser Phe
            180                 185                 190

Val Gly Thr Ala Gln Tyr Val Ser Pro Glu Leu Leu Thr Glu Lys Ser
        195                 200                 205

Ala Cys Lys Ser Ser Asp Leu Trp Ala Leu Gly Cys Ile Ile Tyr Gln
    210                 215                 220

Leu Val Ala Gly Leu Pro Pro Phe Arg Ala Gly Asn Glu Tyr Leu Ile
225                 230                 235                 240

Phe Gln Lys Ile Ile Lys Leu Glu Tyr
                245
```

<210> 5

<211> 8
<212> PRT
<213> Artificial Sequence

<220>
<223> Phosphorylation consensus motif

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<222> (6)..(6)
<223> Any amino acid

<400> 5

Thr Phe Cys Gly Thr Xaa Glu Leu
1 5

<210> 6
<211> 229
<212> PRT
<213> Homo sapiens

<400> 6

Pro Pro Gln Pro Arg Lys Lys Arg Pro Glu Asp Phe Lys Phe Gly Lys
1 5 10 15

Ile Leu Gly Glu Gly Ser Phe Ser Thr Val Val Leu Ala Arg Glu Leu
20 25 30

Ala Thr Ser Arg Glu Tyr Ala Ile Lys Ile Leu Glu Lys Arg His Ile
35 40 45

Ile Lys Glu Asn Lys Val Pro Tyr Val Thr Arg Glu Arg Asp Val Met
50 55 60

Ser Arg Leu Asp His Pro Phe Phe Val Lys Leu Tyr Phe Thr Phe Gln
65 70 75 80

Asp Asp Glu Lys Leu Tyr Phe Gly Leu Ser Tyr Ala Lys Asn Gly Glu
85 90 95

Leu Leu Lys Tyr Ile Arg Lys Ile Gly Ser Phe Asp Glu Thr Cys Thr
100 105 110

Arg Phe Tyr Thr Ala Glu Ile Val Ser Ala Leu Glu Tyr Leu His Gly
115 120 125

```
Lys Gly Ile Ile His Arg Asp Leu Lys Pro Glu Asn Ile Leu Leu Asn
    130                 135                 140

Glu Asp Met His Ile Gln Ile Thr Asp Phe Gly Thr Ala Lys Val Leu
145                 150                 155                 160

Ser Pro Glu Ser Lys Gln Ala Arg Ala Asn Ser Phe Val Gly Thr Ala
                165                 170                 175

Gln Tyr Val Ser Pro Glu Leu Leu Thr Glu Lys Ser Ala Cys Lys Ser
            180                 185                 190

Ser Asp Leu Trp Ala Leu Gly Cys Ile Ile Tyr Gln Leu Val Ala Gly
        195                 200                 205

Leu Pro Pro Phe Arg Ala Gly Asn Glu Tyr Leu Ile Phe Gln Lys Ile
    210                 215                 220

Ile Lys Leu Glu Tyr
225
```

<210> 7
<211> 251
<212> PRT
<213> Artificial Sequence

<220>
<223> Modified PDK1

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Gly Pro Met Asp Gly Thr Ala Ala Glu Pro Arg Pro Gly Ala Gly Ser
1               5                   10                  15

Leu Gln His Ala Gln Pro Pro Pro Gln Pro Arg Lys Lys Arg Pro Glu
            20                  25                  30

Asp Phe Lys Phe Gly Lys Ile Leu Gly Glu Gly Ser Phe Ser Thr Val
        35                  40                  45

Val Leu Ala Arg Glu Leu Ala Thr Ser Arg Glu Tyr Ala Ile Lys Ile
    50                  55                  60

Leu Glu Lys Arg His Ile Ile Lys Glu Asn Lys Val Pro Tyr Val Thr
65                  70                  75                  80
```

```
Arg Glu Arg Asp Val Met Ser Arg Leu Asp His Pro Phe Phe Val Lys
                85                  90                  95

Leu Tyr Phe Thr Phe Gln Asp Asp Glu Lys Leu Tyr Phe Gly Leu Ser
            100                 105                 110

Tyr Ala Lys Asn Gly Glu Leu Leu Lys Tyr Ile Arg Lys Ile Gly Ser
        115                 120                 125

Phe Asp Glu Thr Cys Thr Arg Phe Tyr Thr Ala Glu Ile Val Ser Ala
    130                 135                 140

Leu Glu Tyr Leu His Gly Lys Gly Ile Ile His Arg Asp Leu Lys Pro
145                 150                 155                 160

Glu Asn Ile Leu Leu Asn Glu Asp Met His Ile Gln Ile Thr Asp Phe
                165                 170                 175

Gly Thr Ala Lys Val Leu Ser Pro Glu Ser Lys Gln Ala Arg Ala Asn
            180                 185                 190

Ser Phe Val Gly Thr Ala Gln Tyr Val Ser Pro Glu Leu Leu Thr Glu
        195                 200                 205

Lys Ser Ala Cys Lys Ser Ser Asp Leu Trp Ala Leu Gly Cys Ile Ile
    210                 215                 220

Tyr Gln Leu Val Ala Gly Leu Pro Pro Phe Arg Ala Gly Asn Glu Tyr
225                 230                 235                 240

Leu Ile Phe Gln Lys Ile Ile Lys Leu Glu Tyr
                245                 250
```

<210> 8
<211> 14
<212> PRT
<213> Homo sapiens

<400> 8

```
Lys Val Pro Tyr Val Thr Arg Glu Arg Asp Val Met Ser Arg
1               5                   10
```

<210> 9
<211> 8
<212> PRT
<213> Artificial Sequence

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<221> MISC_FEATURE
<222> (1)..(1)
<223> T or S

<220>
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<222> (6)..(6)
<223> Any residue

<400> 9

Xaa Phe Cys Gly Thr Xaa Glu Leu
1 5

<210> 10
<211> 6
<212> PRT
<213> Artificial Sequence

<220>
<223> PDK2 activity

<220>
<221> MISC_FEATURE
<222> (2)..(3)
<223> Any residue

<220>
<221> MISC_FEATURE
<222> (5)..(5)
<223> S or T

<220>
<221> MISC_FEATURE
<222> (6)..(6)
<223> P or Y

<400> 10

Pro Xaa Xaa Pro Xaa Xaa
1 5

<210> 11
<211> 6
<212> PRT
<213> Artificial Sequence

<220>
<223> Phosphorylated hydrophobic motif

<220>
<221> MISC_FEATURE
<222> (2)..(3)
<223> Any residue

<220>
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<222> (5)..(5)
<223> Any negatively charged residue

<400> 11

Phe Xaa Xaa Phe Xaa Tyr
1 5

<210> 12
<211> 51
<212> PRT
<213> Homo sapiens

<400> 12

Gln Pro Arg Lys Lys Arg Pro Glu Asp Phe Lys Phe Gly Lys Ile Leu
1 5 10 15

Gly Glu Gly Ser Phe Ser Thr Val Val Leu Arg Glu Arg Asp Val Met
20 25 30

Ser Arg Leu Asp His Pro Phe Phe Val Lys Leu Tyr Phe Thr Phe Gln
35 40 45

Asp Asp Glu
50

<210> 13
<211> 51
<212> PRT
<213> Homo sapiens

<400> 13

```
Pro Lys His Arg Val Thr Met Asn Glu Phe Glu Tyr Leu Lys Leu Leu
1               5                   10                  15

Gly Lys Gly Thr Phe Gly Lys Val Ile Leu Thr Glu Asn Arg Val Leu
            20                  25                  30

Gln Asn Ser Arg His Pro Phe Leu Thr Ala Leu Lys Tyr Ser Phe Gln
        35                  40                  45

Thr His Asp
    50
```

<210> 14
<211> 51
<212> PRT
<213> Homo sapiens

<400> 14

```
Gly Pro Glu Lys Ile Arg Pro Glu Cys Phe Glu Leu Leu Arg Val Leu
1               5                   10                  15

Gly Lys Gly Gly Tyr Gly Lys Val Phe Gln Ala Glu Arg Asn Ile Leu
            20                  25                  30

Glu Glu Val Lys His Pro Phe Ile Val Asp Leu Ile Tyr Ala Phe Gln
        35                  40                  45

Thr Gly Gly
    50
```

<210> 15
<211> 52
<212> PRT
<213> Homo sapiens

<400> 15

```
Ser Asn Pro His Ala Lys Pro Ser Asp Phe His Phe Leu Lys Val Ile
1               5                   10                  15

Gly Lys Gly Ser Phe Gly Lys Val Leu Leu Ser Glu Arg Asn Val Leu
            20                  25                  30

Leu Lys Asn Val Lys His Pro Phe Leu Val Gly Leu His Phe Ser Phe
        35                  40                  45
```

Gln Thr Ala Asp
50

<210> 16
<211> 51
<212> PRT
<213> Homo sapiens

<400> 16

Gly Ser Glu Lys Ala Asp Pro Ser His Phe Glu Leu Leu Lys Val Leu
1 5 10 15

Gly Gln Gly Ser Phe Gly Lys Val Phe Leu Met Glu Arg Asp Ile Leu
20 25 30

Ala Asp Val Asn His Pro Phe Val Val Lys Leu His Tyr Ala Phe Gln
35 40 45

Thr Glu Gly
50

<210> 17
<211> 318
<212> PRT
<213> Homo sapiens

<400> 17

Lys Val Phe Gln Val Arg Lys Val Thr Gly Ala Asn Thr Gly Lys Ile
1 5 10 15

Phe Ala Met Lys Val Leu Lys Lys Ala Met Ile Val Arg Asn Ala Lys
20 25 30

Asp Thr Ala His Thr Lys Ala Glu Arg Asn Ile Leu Glu Glu Val Lys
35 40 45

His Pro Phe Ile Val Asp Leu Ile Tyr Ala Phe Gln Thr Gly Gly Lys
50 55 60

Leu Tyr Leu Ile Leu Glu Tyr Leu Ser Gly Gly Glu Leu Phe Met Gln
65 70 75 80

Leu Glu Arg Glu Gly Ile Phe Met Glu Asp Thr Ala Cys Phe Tyr Leu
85 90 95

```
Ala Glu Ile Ser Met Ala Leu Gly His Leu His Gln Lys Gly Ile Ile
            100                 105                 110

Tyr Arg Asp Leu Lys Pro Glu Asn Ile Met Leu Asn His Gln Gly His
        115                 120                 125

Val Lys Leu Thr Asp Phe Gly Leu Cys Lys Glu Ser Ile His Asp Gly
    130                 135                 140

Thr Val Thr His Thr Phe Cys Gly Thr Ile Glu Tyr Met Ala Pro Glu
145                 150                 155                 160

Ile Leu Met Arg Ser Gly His Asn Arg Ala Val Asp Trp Trp Ser Leu
                165                 170                 175

Gly Ala Leu Met Tyr Asp Met Leu Thr Gly Ala Pro Pro Phe Thr Gly
            180                 185                 190
```